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NORDINE CHEIKH

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ARNOLD & PORTER LLP
ATTN: IP DOCKETING DEPT.
555 TWELFTH STREET, N.W.
WASHINGTON, DC 20004-1206

EXAMINER

CLOW, LORI A

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UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE BOARD OF PATENT APPEALS
AND INTERFERENCES

Ex parte NORDINE CHEIKH, DANE K. FISHER, and JINGDONG LIU

Appeal 2008-2045
Application 09/237,183
Technology Center 1600

Decided: September 26, 2008

Before TONI R. SCHEINER, DONALD E. ADAMS, and ERIC GRIMES,
Administrative Patent Judges.

ADAMS, *Administrative Patent Judge.*

DECISION ON APPEAL

This appeal under 35 U.S.C. § 134 involves claims 2 and 7-27, the only claims pending in this application. We have jurisdiction under 35 U.S.C. § 6(b).

INTRODUCTION

The claims are directed to a substantially purified nucleic acid molecule. Claims 2 and 7 are illustrative:

2. A substantially purified nucleic acid molecule that encodes a maize or a soybean enzyme, wherein said nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 11, 446, 935, 1108, 2042, 2166, 2252, 2644, 2681, and 2753, wherein said enzyme encoded by said nucleic acid molecule is triose phosphate isomerase, vacuolar H⁺ translocating-pyrophosphatase, sucrose synthase, hexokinase, fructose 1,6-bisphosphate aldolase, fructose 6-phosphate 2-kinase, invertase, fructokinase, NDP-kinase, and UDP-glucose pyrophosphorylase, respectively.

7. A substantially purified nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 11, 446, 935, 1108, 2042, 2166, 2252, 2644, 2681, and 2753.

The Examiner relies on the following evidence to support the rejections of record.¹

Russell et al., *Structural Features can be Unconserved in Proteins with Similar Folds*, 244 *J. Mol. Biol.* 332-350 (1994).

Gerhold et al., *It's the genes! EST access to human genome content*, 18(12) *BioEssays* 973-981 (1996).

Wells et al., *The chemokine information source: identification and characterization of novel chemokines using the WorldWideWeb and*

¹ The Examiner incorrectly asserts that “[n]o evidence is relied upon by the examiner in the rejection of the claims under appeal” (Ans. 3). The Examiner relies on a number of evidentiary references to support her position (Ans. 9). Appellants’ arguments addressed these references (App. Br. 8). Accordingly, we find the Examiner’s misstatement of the evidence to be a harmless error on this record.

Expressed Sequence Tag Databases, 61(5) *J. Leukocyte Biol.* 545-550 (1997).

Attwood, *The babel of bioinformatics*, 290 *Science* 471-473 (2000).

The rejections as presented by the Examiner are as follows:

Claims 2 and 7-27 stand rejected under 35 U.S.C. § 101 as lacking a patentable utility and under the enablement provision of 35 U.S.C. § 112, first paragraph based on the finding of lack of utility.

We reverse.

DISCUSSION

Claims 2 and 7-27 stand rejected under 35 U.S.C. § 101 as lacking a patentable utility and under the enablement provision of 35 U.S.C. § 112, first paragraph based on the finding of lack of utility.²

The claims are drawn to a substantially purified nucleic acid molecule that encodes a maize or a soybean enzyme. Independent claims 2 and 7 require that the nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of:

a. SEQ ID NO: 11, which encodes for a maize or soybean triose phosphate isomerase enzyme or fragment thereof (Spec. 26);

² The Examiner rejected the claims under both 35 U.S.C. § 101 and 35 U.S.C. § 112, first paragraph. However the rejection for nonenablement was presented simply as a corollary of the finding of lack of utility (*see* Ans. 5). In addition, Appellants rely on their arguments to the rejection under 35 U.S.C. § 101 to rebut the rejection under the enablement provision of 35 U.S.C. § 112, first paragraph. Therefore, although we discuss only the § 101 rejection, our conclusion also applies to the rejection under the enablement provision of 35 U.S.C. § 112, first paragraph.

- b. SEQ ID NO: 446, which encodes for a maize or soybean vacuolar H^+ translocating-pyrophosphatase enzyme or fragment thereof (Spec. 28);
- c. SEQ ID NO: 935, which encodes for a maize or soybean sucrose synthase enzyme or fragment thereof (Spec. 29);
- d. SEQ ID NO: 1108, which encodes for a maize or soybean hexokinase enzyme or fragment thereof (Spec. 30);
- e. SEQ ID NO: 2042, which encodes for a maize or soybean fructose 1,6-biphosphate aldolase enzyme or fragment thereof (Spec. 26);
- f. SEQ ID NO: 2166, which encodes for a maize or soybean fructose 6-phosphate 2-kinase enzyme or fragment thereof (Spec. 27);
- g. SEQ ID NO: 2252, which encodes for a maize or soybean invertase enzyme or fragment thereof (Spec. 29);
- h. SEQ ID NO: 2644, which encodes for a maize or soybean fructokinase enzyme or fragment thereof (Spec. 30);
- i. SEQ ID NO: 2681, which encodes for a maize or soybean NDP-kinase enzyme or fragment thereof (*id.*); and
- j. SEQ ID NO: 2753, which encodes for a maize or soybean UDP-glucose pyrophosphorylase enzyme or fragment thereof (Spec. 32).

Claims 18-27 depend from claim 2. Claims 8-17 depend from claim 7.

As Appellants explain, their Specification discloses that the recited sequences can be used, *inter alia*, “to determine the level or pattern of expression of proteins or mRNAs associated with one of these coding sequences . . . and to overexpress or suppress one or more of these coding sequences in a transgenic plant” (App. Br. 6). According to Appellants, the asserted utilities are specific to the particular nucleic acid sequences listed in

their claims because they are “not shared by any general nucleic acid sequence” (*id.*). In addition, Appellants assert that the utilities are “*substantial* because the Specification as filed provides well-defined and particular benefits, for each of the[] sequences” and “are *well-established* because the proteins encoded by these sequences are well-known” (*id.*).

The Examiner is not persuaded. While Appellants assert that their “specification provides a statistically relevant correlation between the claimed nucleic acid sequences and the respective enzymes” (App. Br. 7), the Examiner asserts that Appellants’ reliance on “BLAST search alignment identity scores” is insufficient to establish that the claimed nucleic acid molecules have the recited enzymatic activity (Ans. 10). According to the Examiner, “one skilled in the art would have reason to doubt that sequence similarity alone would reasonably support the assertion that the biological activity of the claimed subject matter would be the same as that of the similar sequence” (Ans. 8). In support of this assertion, the Examiner relies on Atwood, Gerhold, Wells, and Russell (Ans. 8-9).

The Examiner does not, however, direct our attention to any portion of the cited references that support her position. Our review of the cited references leads us away from the Examiner’s conclusion. For example, Wells teaches that the chemokines family of proteins has been divided into the CXC, CC, and C subfamilies “depending on the spacings of highly characteristic cysteine residues within their amino-terminal regions” (Wells, 545: col. 2, ll. 20-22). Wells teaches that

In addition to the conserved cysteine motif described above, the CC chemokines share other clear sequence similarities such as a C-terminal helix and conserved hydrophobic sequences in the first and third beta sheet. These features make the identification

of novel chemokines in sequence databases relatively easy because even though the overall sequence identity levels between chemokines may be as low as 20%, the cysteine spacings and hydrophobicity may still be used to detect novel chemokine sequences.

(Wells, 545: col. 2, l. 28 - 546: col. 1, l. 6.) Therefore, Wells teaches that despite an overall sequence identity level as low as 20%, the features of the sequences may still be used to detect novel chemokine sequences.³ Further, the Gerhold paper discusses ESTs and teaches that “one can best find proteins related to *ras*, for example, using a protein or DNA sequence query” (Gerhold 975: col. 2, ll. 17-19).

Accordingly, we find that the evidence relied upon by the Examiner fails to support the Examiner’s assertion that “one skilled in the art would have reason to doubt that sequence similarity alone would reasonably support the assertion that the biological activity of the claimed subject matter would be the same as that of the similar sequence” (Ans. 8). Instead, we agree with Appellants’ assertion that “[n]one of the scientific publications set forth by the Examiner undermine the credibility of Appellants’ assertion that the utilities of SEQ ID NOs: 11, 446, 935, 1108, 2042, 2166, 2252, 2644, 2681, and 2753 are specific, substantial, or well-established” (App. Br. 8). Simply stated, the evidence on this record is not sufficient to rebut

³ In contrast to Wells’ observation that sequences with an identity level as low as 20% can be used to identify other chemokine sequences, the Examiner recognizes that the sequences of the claimed nucleic acid molecules are 79-80% identical to a sequence that encodes a specific enzyme as disclosed in Appellants’ Specification (Ans. 7; *see also* Spec. 26-32).

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Appellants' presumptively accurate disclosure. *In re Marzocchi*, 439 F.2d 220, 224 (CCPA 1971).

Accordingly, we reverse the rejection of claims 2 and 7-27 stand rejected under 35 U.S.C. § 101 as lacking a patentable utility and under the enablement provision of 35 U.S.C. § 112, first paragraph based on the finding of lack of utility.

CONCLUSION

In summary, we reverse the rejections of record.

REVERSED

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ARNOLD & PORTER LLP
ATT: IP DOCKETING DEPT.
555 TWELFTH STREET, N.W.
WASHINGTON, DC 20004-1206